

EMBL-EBI		All Databases	Enter Text Here	Go	Reset	Check for updates
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General Help	Formats	EMBOSS Align Results				
Gaps	Matrix	Needle Results				
References	EMBOSS Align Help	Matrix	DNAfull			
		Open gap penalty	10.0			
		Gap extension penalty	0.5			
		Needle output	needle-20110228-0453413765.output			
SUBMIT ANOTHER JOB						

```
#####
# Program: needle
# Rundate: Mon 28 Feb 2011 04:53:41
# Commandline: needle
# [-sequence] /ebi/extserv/old-work/needle-20110228-0453413765.input.1
# [-bsequence] /ebi/extserv/old-work/needle-20110228-0453413765.input.2
# -outfile /ebi/extserv/old-work/needle-20110228-0453413765.output
# -gapopen 10.0
# -gapextend 0.5
# -datafile EDNAFULL
# -sprotein1
# -sprotein2
# -auto
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20110228-0453413765.output
#####

=====
#
# Aligned_sequences: 2
# 1: EMBOS_001
# 2: EMBOS_001
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1180
# Identity: 771/1180 (65.3%) 
# Similarity: 771/1180 (65.3%)
# Gaps: 179/1180 (15.2%)
# Score: 2517.0
#
# =====
```

DNA encoding A26054	EMBOSS_001	1 atggaaagatg-gttaaa-----tct-tctgttgcgt-----	32
		
SEQ ID NO:2	EMBOSS_001	1 -----ATGCCCTCTCAAGCGGATCTCTGTCGCTGGCCCTGGCCAGTC	42
	EMBOSS_001	33 -----tgtttttt-----ttttgt	47
		
	EMBOSS_001	43 GCCTCGGCTCTCCGCTGCTACTCGGGACACCAATGAACCTCTG	92
	EMBOSS_001	48 ttttac-----ggccct-----ggcgccgacaaatgc	76
		
	EMBOSS_001	93 CTTCACCAATGCAATGGCTCAACTCACCAGATGAACACCACTGC	142
	EMBOSS_001	77 cgaacatagtcatctccgaacgggtggatcatcgcgggtccggcgcc	126
		
	EMBOSS_001	143 CGAACGTGACCATTTTCGCAAGGGTGGTACCATCGCGGCTCCGATTCC	192
	EMBOSS_001	127 accggaaaacggacggacggacggactacaaacggccggggactggggatggatgc	176

EMBOSS_001	177 cctcatcaatgcggtgccagaggtaagaactggccatgttaaggcg	226
EMBOSS_001	243 CCTCATCGATGCCGTGCCATCATGCTGGATGTGCCAATGTTGCCGGC	292
EMBOSS_001	227 agcatgtctccaacatggccagcgagaacatgacccgtgacgttgtctt	276
EMBOSS_001	293 TCCAGGTGGCCAACGTGGGAAGCGAGGATATCACCTCTGACATCCTGATT	342
EMBOSS_001	277 aagctgtccacgcgggtgaacgagc-----tgcacgcggacatgt	320
EMBOSS_001	343 TCCATGTCCAAGAACGTGAAAC-CGCCTGTATGAGGACCCGACCA--T	389
EMBOSS_001	321 ggacgggtgtgtcatccccacggcaccgacccgtggaggatctgcct	370
EMBOSS_001	390 GGCGGGTGTGTCATCACCCACGGCACCGACACCCTCGAGGAGACTGCCT	439
EMBOSS_001	371 acttcctgcacctactgtcaaaaatgtacaaggccatgttgcgttgcgt	420
EMBOSS_001	440 TCTCTCTGGACGCCACTGTCAACTGTGGCAAGGCCATTGTCATCGTGGT	489
EMBOSS_001	421 gccatgcggccagcacaaggccatctcagctgacggccatgtaaatctgt	470
EMBOSS_001	490 GCCATGCGCCCATCCACGGCCATCTCAGCTGACGGGCCCTCAATCTGCT	539
EMBOSS_001	471 cgaaggccgtgcgggtgtgtggcacaaggcgtgcgcggcgtgcgggtca	520
EMBOSS_001	540 CGAAGCCGTGACGGTGGCTGCCCCATCGACGGGGGATCGGGTGGCCA	589
EMBOSS_001	521 tgggtgtctcaacgatcgatggctggccgtatataccaaagacc	570
EMBOSS_001	590 TGGTGGTCATGAACGATGCGATCTGGCTCGGCTTAATGTCAGGAAAGACC	639
EMBOSS_001	571 aatgcctccactctggacacccatcaaggccatgaggagggttgcaccc	620
EMBOSS_001	640 AATGCCAACACTATGGACACCTTCAGGCCATGGAGATGGGCTACCTTGG	689
EMBOSS_001	621 cgtatcatcgccaa-cgcatt-----tactacaaaacccgtatcgaca	664
EMBOSS_001	690 CGAGATGATCTAACACCCCTTCTCTTCTAC----CCG-CCGGTCA	733
EMBOSS_001	665 agctgcataccactcggt---cggtttgcgtccggccgtacttc	710
EMBOSS_001	734 AG-----CCAACCGGTAAGGTGGCTTGTACATCACCAACGTGACTGA	776
EMBOSS_001	711 gctcccaaagtggacattctgtatgggtatcaggac---gaccggat	757
EMBOSS_001	777 GATCCCCCGTGGACATCTGTCTTCTTATGAGGACATGACAAACGACA	826
EMBOSS_001	758 acctctacgacgcgcgcattccaggatgtgtcaaggaaattgtatgcc	807
EMBOSS_001	827 CCCTCTACACGCCATC-TCCAG---TGGTGGCCAGGGAAATTGATGGC	873
EMBOSS_001	808 ggatgggtgtgtatccgttca-----gttc---gtgg-tat-----	842
EMBOSS_001	874 GGGGCTGGTGTGGAGGGCTCACAACTCTTCATGAGGCTATCGAGGA	923
EMBOSS_001	843 tggccgcatcgtaaggctatggaaaagggtcggtcatacgagata	892
EMBOSS_001	924 TGTCTCATCAACCG-----TTGGGAGA-----TCCTGTCGTGCAGAGTA	961
EMBOSS_001	893 cgcgcacaggcaatgggatagtggccac---ccgac---gaagacgtccccg	937
EMBOSS_001	962 TGCGCACAGTCATGGGGAAAGTGCCTACTGTCAAGCTGAGCAGCGACACC	1011
EMBOSS_001	938 gcc-----tcgtcagtgtatccctaaacccggcgcatccgcattct	980
EMBOSS_001	1012 GCAACCCACATGCCAGTGGATCTAAACCCGAGAAGTCCCGATCT	1061
DNA encoding A26054	981 gttatgttggcgctaaactc---ggacaag---tgcctaaatgtatccaa	1026

SEQ ID NO:2 EMBOSS_001 1108 GACGTGTTGCTCTGGGCACGGATGCGTAG 1137

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